CRF Errors Corrected by the STIC Systems Branch

Serial Numbr: 09/771,904

ENTERED

CRF Processing Date: 2/21/2002
Edited by: ___
Vrified by: ___

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

☐ Edited the Current Application Data section with the actual current number. The number input by the applicant was ☐ the prior application data; or ☐ other _____

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☑ Other: Seq 64 - aligned amino acid nos.
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

OIPE

P.S

```
 4 <110> APPLICANT: DeBonte, Lorin R.
 5         Fan, Zhegong
 6         Miao, Guo-Hua
 8 <120> TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
10 <130> FILE REFERENCE: 07148-063003
12 <140> CURRENT APPLICATION NUMBER: US 09/771,904
13 <141> CURRENT FILING DATE: 2001-01-29
15 <150> PRIOR APPLICATION NUMBER: US 08/874,109
16 <151> PRIOR FILING DATE: 1997-06-12
18 <160> NUMBER OF SEQ ID NOS: 69
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1155
24 <212> TYPE: DNA
25 <213> ORGANISM: Brassica napus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)...(1152)
30 <223> OTHER INFORMATION: Wild type Fad2
32 <221> NAME/KEY: misc_feature
33 <222> LOCATION: 205
34 <223> OTHER INFORMATION: n = a, g, c, or t/u
36 <400> SEQUENCE: 1
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38 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
39  1               5                  10                  15
41 gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act          96
42 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
43              20                  25                  30
45 gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg         144
46 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
47          35                  40                  45
49 atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc         192
50 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
51      50                  55                  60
53 tgc ttc tac tac ntc gcc acc act tac ttc cct ctc ctc cct cac cct         240
54 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
55  65                  70                  75                  80
57 ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc         288
58 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
59                  85                  90                  95
61 cta acc ggc gtc tgg gtc ata gcc cac gaa tgc ggc cac cac gcc ttc         336
62 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
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RAW SEQUENCE LISTING   DATE: 02/21/2002
PATENT APPLICATION: US/09/771,904   TIME: 08:14:45

Input Set : A:\PTO.txt
Output Set: N:\CRF3\02212002\I771904.raw

```
63              100             105             110
65 agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc      384
66 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
67         115             120             125
69 ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cgc agc cac      432
70 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
71     130             135             140
73 cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag      480
74 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
75 145             150             155             160
77 aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg      528
78 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
79             165             170             175
81 gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg      576
82 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
83         180             185             190
85 tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc cgt      624
86 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
87         195             200             205
89 tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc      672
90 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
91     210             215             220
93 cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc      720
94 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
95 225             230             235             240
97 ttc cgt tac gcc gcc ggc cag gga gtg gcc tcg atg gtc tgc ttc tac      768
98 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
99             245             250             255
101 gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac     816
102 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
103             260             265             270
105 ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg     864
106 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
107         275             280             285
110 gat tgg ttc agg gga gct ttg gct acc gtt gac aga gac tac gga atc     912
111 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
112     290             295             300
114 ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcc cat cat     960
115 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
116 305             310             315             320
118 ccg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg     1008
119 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
120             325             330             335
122 ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg     1056
123 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
124             340             345             350
126 gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg     1104
127 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
128         355             360             365
```

```
130 gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta          1152
131 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
132         370             375             380
134 tga                                                                      1155
136 <210> SEQ ID NO: 2
137 <211> LENGTH: 384
138 <212> TYPE: PRT
139 <213> ORGANISM: Brassica napus
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Xaa = Phe, Leu, Ile, or Val
144 <400> SEQUENCE: 2
145 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
146   1               5               10              15
147 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
148         20              25              30
149 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
150         35              40              45
151 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
152     50              55              60
153 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
154   65              70              75              80
155 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
156             85              90              95
157 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
158         100             105             110
159 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
160         115             120             125
161 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
162     130             135             140
164 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
165 145             150             155             160
166 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
167             165             170             175
168 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
169             180             185             190
170 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
171         195             200             205
172 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
173         210             215             220
174 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
175 225             230             235             240
176 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
177             245             250             255
178 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
179             260             265             270
180 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
181         275             280             285
182 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
183     290             295             300
```

```
184 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
185- 305                     310                 315                 320
186 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
187                 325                 330                 335
188 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
189                 340                 345                 350
190 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
191             355                 360                 365
192 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
193         370                 375                 380
195 <210> SEQ ID NO: 3
196 <211> LENGTH: 1155
197 <212> TYPE: DNA
198 <213> ORGANISM: Brassica napus
200 <220> FEATURE:
201 <221> NAME/KEY: CDS
202 <222> LOCATION: (1)...(1152)
203 <223> OTHER INFORMATION: G to A transversion mutation at nucleotide 316
205 <221> NAME/KEY: misc_feature
206 <222> LOCATION: 205
207 <223> OTHER INFORMATION: n = a, g, c, or t/u
209 <400> SEQUENCE: 3
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211 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
212   1               5                   10                  15
214 gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act     96
215 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
216             20                  25                  30
218 gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg    144
219 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
220         35                  40                  45
222 atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc    192
223 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
224         50                  55                  60
226 tgc ttc tac tac ntc gcc acc act tac ttc cct ctc ctc cct cac cct    240
227 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
228   65                  70                  75                  80
230 ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc    288
231 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
232                 85                  90                  95
234 cta acc ggc gtc tgg gtc ata gcc cac aag tgc ggc cac cac gcc ttc    336
235 Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe
236                 100                 105                 110
238 agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc    384
239 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
240             115                 120                 125
242 ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cgc agc cac    432
243 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
244         130                 135                 140
```

```
        Input Set : A:\PTO.txt
        Output Set: N:\CRF3\02212002\I771904.raw

246 cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag        480
247.His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
248 145                     150                 155                 160
250 aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg        528
251 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
252                 165                 170                 175
254 gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg        576
255 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
256                 180                 185                 190
258 tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc cgt        624
259 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
260             195                 200                 205
262 tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc        672
263 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
264     210                 215                 220
266 cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc        720
267 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
268 225                 230                 235                 240
272 ttc cgt tac gcc gcc ggc cag gga gtg gcc tcg atg gtc tgc ttc tac        768
273 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
274                 245                 250                 255
276 gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac        816
277 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
278                 260                 265                 270
280 ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg        864
281 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
282             275                 280                 285
284 gat tgg ttc agg gga gct ttg gct acc gtt gac aga gac tac gga atc        912
285 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
286     290                 295                 300
288 ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcc cat cat        960
289 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
290 305                 310                 315                 320
292 ccg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg       1008
293 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
294                 325                 330                 335
296 ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg       1056
297 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
298             340                 345                 350
300 gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg       1104
301 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
302             355                 360                 365
304 gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta       1152
305 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
306     370                 375                 380
308 tga                                                                  1155
310 <210> SEQ ID NO: 4
311 <211> LENGTH: 384
312 <212> TYPE: PRT
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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/771,904

DATE: 02/21/2002
TIME: 08:14:46

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\02212002\I771904.raw**

```
L:53  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:54  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:153 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:153 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:328 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:328 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
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